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Application No: 07110791 Version No: 1.0

Input Set:

Output Set:

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No. of SeqIDs Defined: 4
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<110> The United States of America, as represented by the
Secretary, Department of Health and Human Services
King, C. Richter
Kraus, Matthias H.
Aaronson, Stuart A.

<120> HUMAN GENE RELATED TO BUT DISTINCT FROM EGF RECEPTOR GENE

<130> 6137NCI-24

<140> 07110791

<141> 2010-01-15

<160> 4

<170> PatentIn version 3.5

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<211> 78

<212> PRT

<213> Homo sapiens

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Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu	
1 5 10	
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Leu Ala Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val	
15 20 25 30	
tgc caa ggc acg agt aac aag ctc acg cag ttg ggc act ttt gaa gat	324
Cys Gln Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp	
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cat ttt ctc agc ctc cag agg atg ttc aat aac tgt gag gtg gtc ctt	372
His Phe Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu	
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Gly Asn Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe	
65 70 75	
tta aag acc atc cag gag gtg gct ggt tat gtc ctc att gcc ctc aac	468
Leu Lys Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn	
80 85 90	
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Thr Val Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn	
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cat act cct cct ctg gat cca cag gaa ctg gat att ctg aaa acc gta His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val 385 390 395	1380
aag gaa atc aca ggg ttt ttg ctg att cag gct tgg cct gaa aac agg Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg 400 405 410	1428
acg gac ctc cat gcc ttt gag aac cta gaa atc ata cgc ggc agg acc Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr 415 420 425 430	1476
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Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His			
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Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu			
595	600	605	
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Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro			
610	615	620	
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Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr			
625	630	635	
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Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu			
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ctc ttg ctg ctg gtg gtg gcc ctg ggg atc ggc ctc ttc atg cga agg			2196
Leu Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg			
655	660	665	670
cgc cac atc gtt ccg aag cgc acg ctg ccg agg ctg ctg cag gag agg			2244
Arg His Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg			
675	680	685	
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Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala			
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Leu Leu Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu			
705	710	715	
ggc tcc ggt gcg ttc ggc acg gtg tat aag gga ctc tgg atc cca gaa			2388
Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu			
720	725	730	
ggt gag aaa gtt aaa att ccc gtc gct atc aag gaa tta aga gaa gca			2436
Gly Glu Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala			
735	740	745	750
aca tct ccg aaa gcc aac aag gaa atc ctc gat gaa gcc tac gtg atg			2484
Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met			
755	760	765	
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Ala Ser Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu			
770	775	780	
acc tcc acc gtg caa ctc atc acg cag ctc atg ccc ttc ggc tgc ctc			2580
Thr Ser Thr Val Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu			

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ctc aac tgg tgt gtg cag atc gca aag ggc atg aac tac ttg gag gac Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp 815	820	825	2676
cgt cgc ttg gtg cac cgc gac ctg gca gcc agg aac gta ctg gtg aaa Arg Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys 835	840	845	2724
aca ccg cag cat gtc aag atc aca gat ttt ggg ctg gcc aaa ctg ctg Thr Pro Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu 850	855	860	2772
ggt gcg gaa gag aaa gaa tac cat gca gaa gga ggc aaa gtg cct atc Gly Ala Glu Glu Lys Glu Tyr His Ala Glu Gly Lys Val Pro Ile 865	870	875	2820
aag tgg atg gca ttg gaa tca att tta cac aga atc tat acc cac cag Lys Trp Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln 880	885	890	2868
agt gat gtc tgg agc tac ggg gtg acc gtt tgg gag ttg atg acc ttt Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe 895	900	905	2916
gga tcc aag cca tat gac gga atc cct gcc agc gag atc tcc tcc atc Gly Ser Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile 915	920	925	2964
ctg gag aaa gga gaa cgc ctc cct cag cca ccc ata tgt acc atc gat Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp 930	935	940	3012
gtc tac atg atc atg gtc aag tgc tgg atg ata gac gca gat agt cgc Val Tyr Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg 945	950	955	3060
cca aag ttc cgt gag ttg atc atc gaa ttc tcc aaa atg gcc cga gac Pro Lys Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp 960	965	970	3108
ccc cag cgc tac ctt gtc att cag ggg gat gaa aga atg cat ttg cca Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro 975	980	985	3156
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Ser Leu Ser Ala	Thr Ser Asn Asn Ser	Thr Val Ala Cys Ile	Asp	
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Arg Asn Gly Leu	Gln Ser Cys Pro Ile	Lys Glu Asp Ser Phe	Leu	
1055	1060	1065		
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Gln Arg Tyr Ser	Ser Asp Pro Thr Gly	Ala Leu Thr Glu Asp	Ser	
1070	1075	1080		